

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/647, 072 A
Source: IFW0
Date Processed by STIC: 03/10/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 03/10/2006

PATENT APPLICATION: US/10/647,072A

TIME: 15:31:45

Input Set : E:\substi SEQLIST 7853-267.TXT

Output Set: N:\CRF4\03092006\J647072A.raw

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4 <110> APPLICANT: Kroczek, Richard
6 <120> TITLE OF INVENTION: COSTIMULATING POLYPEPTIDE OF T CELLS,
7   MONOCLONAL ANTIBODIES, AND THE PREPARATION AND USE THEREOF
10 <130> FILE REFERENCE: 7853-267-999
12 <140> CURRENT APPLICATION NUMBER: 10/647,072A
13 <141> CURRENT FILING DATE: 2003-08-22
15 <150> PRIOR APPLICATION NUMBER: 09/509,283
16 <151> PRIOR FILING DATE: 2000-08-11
18 <150> PRIOR APPLICATION NUMBER: PCT/DE98/02896
19 <151> PRIOR FILING DATE: 1998-09-23
21 <150> PRIOR APPLICATION NUMBER: DE 19821060.4
22 <151> PRIOR FILING DATE: 1998-05-11
24 <150> PRIOR APPLICATION NUMBER: DE 19741929.1
25 <151> PRIOR FILING DATE: 1997-09-23
27 <160> NUMBER OF SEQ ID NOS: 7
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 2641
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (68)...(667)
40 <220> FEATURE:
41 <223> OTHER INFORMATION: 8F4 DNA sequence
43 <400> SEQUENCE: 1
44 cgagagcctg aattcactgt cagctttgaa cactgaacgc gaggactgtt aactgtttct 60
45 ggcaaac atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc 109
46 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg
47 1 5 10
49 att aaa gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg 157
50 Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met
51 15 20 25 30
53 ttt ata ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac 205
54 Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp
55 35 40 45
57 att gtc cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc 253
58 Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu
59 50 55 60
61 tgc gat ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag 301
62 Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys
63 65 70 75
65 agt ctg aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt 349

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```

66 Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe
67      80      85      90
69 ttt cta tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac 397
70 Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn
71 95      100      105      110
73 cta tca att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga 445
74 Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly
75      115      120      125
77 tat ttg cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg 493
78 Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp
79      130      135      140
81 tta ccc ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc 541
82 Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys
83      145      150      155
85 ata ctt att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac 589
86 Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His
87      160      165      170
89 gac cct aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa 637
90 Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys
91 175      180      185      190
93 aaa tct aga ctc aca gat gtg acc cta taa tatggaactc tggcaccag 687
94 Lys Ser Arg Leu Thr Asp Val Thr Leu *
95      195
97 gcatgaagca cggtggccag ttttctctcaa cttgaagtgc aagattctct tatttccggg 747
98 accacggaga gtctgactta actacatata tcttctgctg gtgttttggt caatctggaa 807
99 gaatgactgt atcagtcagt ggggatttta acagactgcc ttggtactgc cgagtctct 867
100 caaaacaaac accctcttgc aaccagcttt ggagaaagcc cagctcctgt gtgctcactg 927
101 ggagtggaaat ccctgtctcc acatctgctc ctagcagtgc atcagccagt aaaacaaaca 987
102 catttacaag aaaaatgttt taaagatgcc aggggtactg aatctgcaaa gcaaatgagc 1047
103 agccaaggac cagcatctgt ccgcatctca ctatcatact acctcttctt tctgtaggga 1107
104 tgagaatttc tcttttaatc agtcaaggga gatgcttcaa agctggagct attttatttc 1167
105 tgagatgttg atgtgaactg tacattagta cactactcagt actctccttc aattgctgaa 1227
106 cccagttga ccattttacc aagacttttag atgctttctt gtgccctcaa ttttcttttt 1287
107 aaaaatactt ctacatgact gcttgacagc ccaacagcca ctctcaatag agagctatgt 1347
108 cttacattct ttcctctgct gctcaatagt tttatatatc tatgcataca tatatacaca 1407
109 catatgtata taaaattcat aatgaatata tttgcctata ttctccctac aagaatattt 1467
110 ttgctccaga aagacatgtt cttttctcaa attcagttaa aatggtttac tttgttcaag 1527
111 ttagtggtag gaaacattgc ccggaattga aagcaaattt attttattat cctattttct 1587
112 accattatct atgttttcat ggtgctatta attacaagtt tagttctttt tgtagatcat 1647
113 attaaaattg caaacaattt catctttaat gggccagcat tctcatggg tagagcagaa 1707
114 tattcattta gcctgaaagc tgcagttact ataggttgct gtcagactat acccatgggtg 1767
115 cctctgggct tgacaggtca aaatggtccc catcagcctg gagcagccct ccagacctgg 1827
116 gtggaattcc aggggttgaga gactccctg agccagaggc cactaggtat tcttgctccc 1887
117 agaggctgaa gtcaccctgg gaatcacagt ggtctacctg cattcataat tccaggatct 1947
118 gtgaagagca catatgtgtc agggcacaat tccctctcat aaaaaccaca cagcctggaa 2007
119 attggcctg gcccttcaag atagccttct ttagaatatg atttggttag aaagattctt 2067
120 aaatatgtgg aatatgatta ttcttagctg gaatatctt tctacttct gtctgcatgc 2127
121 ccaaggcttc tgaagcagcc aatgtcgatg caacaacatt tgtaacttta ggtaaaactgg 2187
122 gattatgttg tagtttaaca ttttgtaact gtgtgcttat agtttacaag tgagaccgca 2247

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Input Set : E:\substi SEQLIST 7853-267.TXT

Output Set: N:\CRF4\03092006\J647072A.raw

```

123 tatgtcatta tgcatactta tattatctta agcatgtgta atgctggatg tgtacagtac 2307
124 agtactgaac ttgtaatttg aatctagtat ggtgttctgt tttcagctga cttggacaac 2367
125 ctgactggct ttgcacaggt gttccctgag ttgtttgcag gtttctgtgt gtgggggtggg 2427
126 gtatggggag gagaaccttc atgggtggccc acctggcctg gttgtccaag ctgtgcctcg 2487
127 acacatcctc atccccagca tgggacacct caagatgaat aataattcac aaaatttctg 2547
128 tgaaatcaaa tccagtttta agaggagcca cttatcaaag agattttaac agtagtaaga 2607
129 aggcaaagaa taaacatttg atattcagca actg 2641
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 199
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
137 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
138 1 5 10 15
139 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
140 20 25 30
141 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
142 35 40 45
143 Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
144 50 55 60
145 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
146 65 70 75 80
147 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
148 85 90 95
149 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
150 100 105 110
151 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
152 115 120 125
153 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
154 130 135 140
155 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
156 145 150 155 160
157 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
158 165 170 175
159 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
160 180 185 190
161 Arg Leu Thr Asp Val Thr Leu
162 195
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 17
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Degenerate oligonucleotide
173 <220> FEATURE:
174 <221> NAME/KEY: misc_feature
175 <222> LOCATION: 3, 9, 15
176 <223> OTHER INFORMATION: n = A,T,C or G
178 <400> SEQUENCE: 3

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W--> 179 mgncttsacng aygtnac 17
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 17
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Degenerate oligonucleotide
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: 3, 9, 15
192 <223> OTHER INFORMATION: n = A,T,C or G
194 <400> SEQUENCE: 4
W--> 195 mgnytdacng aygtnac 17
197 <210> SEQ ID NO: 5
198 <211> LENGTH: 7
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <220> FEATURE:
203 <223> OTHER INFORMATION: peptide found in 8F4-29 kDa sample
205 <220> FEATURE:
206 <221> NAME/KEY: VARIANT
207 <222> LOCATION: 1
208 <223> OTHER INFORMATION: Xaa = Any Amino Acid
210 <400> SEQUENCE: 5
W--> 211 Xaa Arg Leu Thr Asp Val Thr
212 1 5
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 6
217 <212> TYPE: PRT
218 <213> ORGANISM: Homo sapiens
220 <400> SEQUENCE: 6
221 Phe Asp Pro Pro Pro Phe
222 1 5
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 4
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 7
231 Tyr Met Phe Met
232 1

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/10/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3, 9, 15

Seq#:4; N Pos. 3, 9, 15

Seq#:5; Xaa Pos. 1

VERIFICATION SUMMARY

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L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0

L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0